



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

10/785,452
FFW0
7/25/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/785,452

DATE: 07/22/2004

TIME: 09:58:13

Input Set : D:\CFR sequence listing.txt

Output Set: N:\CRF4\07222004\J785452.raw

4 <110> APPLICANT: Tillet, D
 5 Thomas, T
 7 <120> TITLE OF INVENTION: A method of sequestering and/or purifying a polypeptide
 W--> 0 <130> FILE REFERENCE:
 9 <140> CURRENT APPLICATION NUMBER: 10/785,452
 11 <141> CURRENT FILING DATE: 2004-02-25
 13 <150> PRIOR APPLICATION NUMBER: Australia PCT/AU02/01159
 W--> 14 Australia 2002322186 delete
 16 <151> PRIOR FILING DATE: 2002-08-27 delete
 18 <160> NUMBER OF SEQ ID NOS: 12

ERRORED SEQUENCES

20 <210> SEQ ID NO: 1
 22 <211> LENGTH: 714
 24 <212> TYPE: DNA
 26 <213> ORGANISM: Aequorea victoria
 E--> 28 <400> SEQUENCE: -PIS insert response- ①
 29 atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt 45
 30 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 31 1 5 10 15
 33 gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtc agt 90
 34 Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
 35 20 25 30
 37 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa 135
 38 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 39 35 40 45
 41 ttt att tgc act act ggg aag cta cct gtt cca tgg cca aca ctt 180
 42 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
 43 50 55 60
 45 gtc act act ttc gcg tat ggt ctt caa tgc ttt gcg aga tac cca 225
 46 Val Thr Thr Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
 47 65 70 75
 49 gat cat atg aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa 270
 50 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
 51 80 85 90
 53 ggt tat gta cag gaa aga act ata ttt tac aaa gat gac ggg aac 315
 54 Gly Tyr Val Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn
 55 95 100 105
 57 tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt 360
 58 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 59 110 115 120

Does Not Comply
 Corrected Diskette Needed
 (pg. 1-2, 4-11)

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```

61 aat aga atc gag tta aaa ggt att gat ttt aaa gaa gat gga aac 405
62 Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
63      125      130      135
65 att ctt gga cac aaa atg gaa tac aac tat aac tca cat aat gta 450
66 Ile Leu Gly His Lys Met Glu Tyr Asn Tyr Asn Ser His Asn Val
67      140      145      150
69 tac atc atg gca gac aaa cca aag aat gga atc aaa gtt aac ttc 495
70 Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly Ile Lys Val Asn Phe
71      155      160      165
73 aaa att aga cac aac att aaa gat gga agc gtt caa tta gca gac 540
74 Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val Gln Leu Ala Asp
75      170      175      180
77 cat tat caa caa aat act cca att ggc gat ggc cct gtc ctt tta 585
78 His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
79      185      190      195
81 cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcc aaa gat 630
82 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp
83      200      205      210
85 ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta aca 675
86 Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val Thr
87      215      220      225
89 gct gct ggg att aca cat ggc atg gat gaa cta tac aaa 714
90 Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
91      230      235      238

```

95 <210> SEQ ID NO: 2

97 <211> LENGTH: 1149

99 <212> TYPE: DNA

101 <213> ORGANISM: Escherichia coli

E--> 103 <400> SEQUENCE: - pls insert response - 2

```

104 atg ttt gaa cca atg gaa ctt acc aat gac gcg gtg att aaa gtc 45
105 Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val
106 1      5      10      15
108 atc ggc gtc ggc ggc ggc ggc ggt aat gct gtt gaa cac atg gtg 90
109 Ile Gly Val Gly Gly Gly Gly Gly Asn Ala Val Glu His Met Val
110      20      25      30
112 cgc gag cgc att gaa ggt gtt gaa ttc ttc gcg gta aat acc gat 135
113 Arg Glu Arg Ile Glu Gly Val Glu Phe Ala Val Asn Thr Asp
114      35      40      45
116 gca caa gcg ctg cgt aaa aca gcg gtt gga cag acg att caa atc 180
117 Ala Gln Ala Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile
118      50      55      60
120 ggt agc ggt atc acc aaa gga ctg ggc gct ggc gct aat cca gaa 225
121 Gly Ser Gly Ile Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu
122      65      70      75
124 gtt ggc cgc aat gcg gct gat gag gat cgc gat gca ttg cgt gcg 270
125 Val Gly Arg Asn Ala Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala
126      80      85      90
128 gcg ctg gaa ggt gca gac atg gtc ttt att gct gcg ggt atg ggt 315
129 Ala Leu Glu Gly Ala Asp Met Val Phe Ile Ala Ala Gly Met Gly

```

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```

130          95          100          105
132 ggt ggt acc ggt aca ggt gcg gca cca gtc gtc gct gaa gtg gca 360
133 Gly Gly Thr Gly Thr Gly Ala Ala Pro Val Val Ala Glu Val Ala
134          110          115          120
136 aaa gat ttg ggt atc ctg acc gtt gct gtc gtc act aag cct ttc 405
137 Lys Asp Leu Gly Ile Leu Thr Val Ala Val Val Thr Lys Pro Phe
138          125          130          135
142 aac ttt gaa ggc aag aag cgt atg gca ttc gcg gag cag ggg atc 450
143 Asn Phe Glu Gly Lys Lys Arg Met Ala Phe Ala Glu Gln Gly Ile
144          140          145          150
146 act gaa ctg tcc aag cat gtg aac tct ctg atc act atc ccg aac 495
147 Thr Glu Leu Ser Lys His Val Asn Ser Leu Ile Thr Ile Pro Asn
148          155          160          165
150 gac aaa ctg ctg aaa gtt ctg ggc cgc ggt atc tcc ctg ctg gat 540
151 Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile Ser Leu Leu Asp
152          170          175          180
154 gcg ttt ggc gca gcg aac gat gta ctg aaa ggc gct gtg caa ggt 585
155 Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala Val Gln Gly
156          185          190          195
158 atc gct gaa ctg att act cgt ccg ggt ttg atg aac gtg gac ttt 630
159 Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val Asp Phe
160          200          205          210
162 gca gac gta cgc acc gta atg tct gag atg ggc cac gca atg atg 675
163 Ala Asp Val Arg Thr Val Met Ser Glu Met Gly His Ala Met Met
164          215          220          225
166 ggt tct ggc gtg gcg agc ggt gaa gac cgt gcg gaa gaa gct gct 720
167 Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
168          230          235          240
170 gaa atg gct atc tct tct ccg ctg ctg gaa gat atc gac ctg tct 765
171 Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser
172          245          250          255
174 ggc gcg cgc ggc gtg ctg gtt aac atc acg gcg ggc ttc gac ctg 810
175 Gly Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu
176          260          265          270
178 cgt ctg gat gag ttc gaa acg gta ggt aac acc atc cgt gca ttt 855
179 Arg Leu Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe
180          275          280          285
182 gct tcc gac aac gcg act gtg gtt atc ggt act tct ctt gac ccg 900
183 Ala Ser Asp Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro
184          290          295          300
186 gat atg aat gac gag ctg cgc gta acc gtt gtt gcg aca ggt atc 945
187 Asp Met Asn Asp Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile
188          305          310          315
190 ggc atg gac aaa cgt cct gaa atc act ctg gtg acc aat aag cag 990
191 Gly Met Asp Lys Arg Pro Glu Ile Thr Leu Val Thr Asn Lys Gln
192          320          325          330
194 gtt cag cag cca gtg atg gat cgc tac cag cag cat ggg atg gct 1035
195 Val Gln Gln Pro Val Met Asp Arg Tyr Gln Gln His Gly Met Ala
196          335          340          345

```

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198 ccg ctg acc caa gag cag aag ccg gtt gct aaa gtc gtg aat gac 1080
 199 Pro Leu Thr Gln Glu Lys Pro Val Ala Lys Val Val Asn Asp
 200 350 355 360
 202 aat gcg ccg caa act gcg aaa gag ccg gat tat ctg gat atc cca 1125
 203 Asn Ala Pro Gln Thr Ala Lys Glu Pro Asp Tyr Leu Asp Ile Pro
 204 365 370 375

E--> 206 gca ttc ctg cgt aag gln ala asp 1149 SPACE OVER → 1149

W--> 207 Ala Phe Leu Arg Lys CAA GCT GAT

208 380 383

212 <210> SEQ ID NO 3

214 <211> LENGTH: 546

216 <212> TYPE: DNA

218 <213> ORGANISM: Human rhinovirus

E--> 220 <400> SEQUENCE: PLS insert response 3

221 gga cca aac aca gaa ttt gca cta tcc ctg tta agg aaa aac ata 45

222 Gly Pro Asn Thr Glu Phe Ala Leu Ser Leu Leu Arg Lys Asn Ile

223 1 5 10 15

225 atg act ata aca acc tca aag gga gag ttc aca ggg tta ggc ata 90

226 Met Thr Ile Thr Ser Lys Gly Glu Phe Thr Gly Leu Gly Ile

227 20 25 30

229 cat gat cgt gtc tgt gtg ata ccc aca cac gca cag cct ggt gat 135

230 His Asp Arg Val Cys Val Ile Pro Thr His Ala Gln Pro Gly Asp

231 35 40 45

233 gat gta cta gtg aat ggt cag aaa att aga gtt aag gat aag tac 180

234 Asp Val Leu Val Asn Gly Gln Lys Ile Arg Val Lys Asp Lys Tyr

235 50 55 60

237 aaa tta gta gat cca gag aac att aat cta gag ctt aca gtg ttg 225

238 Lys Leu Val Asp Pro Glu Asn Ile Asn Leu Glu Leu Thr Val Leu

239 65 70 75

241 act tta gat aga aat gaa aaa ttc aga gat atc agg gga ttt ata 270

242 Thr Leu Asp Arg Asn Glu Lys Phe Arg Asp Ile Arg Gly Phe Ile

243 80 85 90

245 tca gaa gat cta gaa ggt gtg gat gcc act ttg gta gta cat tca 315

246 Ser Glu Asp Leu Glu Gly Val Asp Ala Thr Leu Val Val His Ser

247 95 100 105

249 aat aac ttt acc aac act atc tta gaa gtt ggc cct gta aca atg 360

250 Asn Asn Phe Thr Asn Thr Ile Leu Glu Val Gly Pro Val Thr Met

251 110 115 120

253 gca gga ctt att aat ttg agt agc acc ccc act aac aga atg att 405

254 Ala Gly Leu Ile Asn Leu Ser Ser Thr Pro Thr Asn Arg Met Ile

255 125 130 135

259 cgt tat gat tat gca aca aaa act ggg cag tgt gga ggt gtg ctg 450

260 Arg Tyr Asp Tyr Ala Thr Lys Thr Gly Gln Cys Gly Gly Val Leu

261 140 145 150

263 tgt gct act ggt aag atc ttt ggt att cat gtt ggc ggt aat gga 495

264 Cys Ala Thr Gly Lys Ile Phe Gly Ile His Val Gly Gly Asn Gly

265 155 160 165

267 aga caa gga ttt tca gct caa ctt aaa aaa caa tat ttt gta gag 540

268 Arg Gln Gly Phe Ser Ala Gln Leu Lys Lys Gln Tyr Phe Val Glu

PLS place the amino acids over the nucleotides. For ex: caa gct gat = Gln Ala Asp

pls explain "N" locations. pls see error explanation on page 8.
 pls convert to lowercase

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convert to all lowercase

269 170 175 180
 C--> 271 aaa caa 546 *Space over* → 546
 272 Lys Gln
 273 182
 277 <210> SEQ ID NO: 4
 279 <211> LENGTH: 27
 281 <212> TYPE: DNA
 C--> 283 <213> ORGANISM: artificial sequence
 W--> 285 <220> FEATURE:
 W--> 285 <223> OTHER INFORMATION:
 E--> 285 <400> SEQUENCE: 4
 287 atcatgagta aaggagaaga acttttc 27
 291 <210> SEQ ID NO: 5
 293 <211> LENGTH: 29
 295 <212> TYPE: DNA
 C--> 297 <213> ORGANISM: artificial sequence
 W--> 299 <220> FEATURE:
 W--> 299 <223> OTHER INFORMATION:
 E--> 299 <400> SEQUENCE: 5
 300 aggatcctta ttgtatagt tcatccatg 29
 304 <210> SEQ ID NO: 6
 306 <211> LENGTH: 24
 308 <212> TYPE: DNA
 C--> 310 <213> ORGANISM: artificial sequence
 W--> 312 <220> FEATURE:
 W--> 312 <223> OTHER INFORMATION:
 E--> 312 <400> SEQUENCE: 6
 313 ggcataatgtt tgaaccaatg gaac 24
 317 <210> SEQ ID NO: 7
 319 <211> LENGTH: 27
 321 <212> TYPE: DNA
 C--> 323 <213> ORGANISM: artificial sequence
 W--> 325 <220> FEATURE:
 W--> 325 <223> OTHER INFORMATION:
 E--> 325 <400> SEQUENCE: 7
 326 gtccatgggc ccttgaaata gtacttc 27
 330 <210> SEQ ID NO: 8
 332 <211> LENGTH: 43
 334 <212> TYPE: DNA
 C--> 336 <213> ORGANISM: artificial sequence
 W--> 338 <220> FEATURE:
 W--> 338 <223> OTHER INFORMATION:
 E--> 338 <400> SEQUENCE: 8
 339 gggcccttga aatagtactt ctatgcagc ttgcttacgc agg 43
 343 <210> SEQ ID NO: 9
 345 <211> LENGTH: 27
 347 <212> TYPE: DNA
 C--> 349 <213> ORGANISM: artificial sequence
 W--> 351 <220> FEATURE:

*mandatory, if <213>
 is artificial/unknown
 please explain in
 section <220> -
 <223>.*

*The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.*

*↑ PLS see error explanation on
 PAGE 7.*

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Input Set : D:\CFR sequence listing.txt

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W--> 351 <223> OTHER INFORMATION: - Same error
 E--> 351 <400> SEQUENCE: 9 <pls insert
 352 cgccatggga ccaaacacag aatttgc 27
 356 <210> SEQ ID NO: 10
 358 <211> LENGTH: 32
 360 <212> TYPE: DNA - Same error
 C--> 362 <213> ORGANISM: artificial sequence
 W--> 364 <220> FEATURE:
 W--> 364 <223> OTHER INFORMATION:
 E--> 364 <400> SEQUENCE: 10 <pls insert
 365 gcggatccct attgtttctc tacaaaatat tg 32
 369 <210> SEQ ID NO: 11
 371 <211> LENGTH: 24
 373 <212> TYPE: DNA - Same error
 C--> 375 <213> ORGANISM: artificial sequence
 W--> 377 <220> FEATURE:
 W--> 377 <223> OTHER INFORMATION:
 E--> 377 <400> SEQUENCE: 11 <pls insert
 378 ggcataatggt tgaaccaatg gaac 24
 382 <210> SEQ ID NO: 12
 384 <211> LENGTH: 25
 386 <212> TYPE: DNA - Same error
 C--> 388 <213> ORGANISM: artificial sequence
 W--> 390 <220> FEATURE:
 W--> 390 <223> OTHER INFORMATION:
 E--> 390 <400> SEQUENCE: 12 <pls insert
 391 cgccatggca gcttgcttac gcagg 25

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : D:\CFR sequence listing.txt

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Use of <220> Feature(NEW RULES):

Error Explanation: ✓

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:4,5,6,7,8,9,10,11,12

VARIABLE LOCATION SUMMARY

DATE: 07/22/2004

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Input Set : D:\CFR sequence listing.txt

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Use of n's or Xaa's (NEW RULES): Error explanation: 2
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:2; N Pos. 1142

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/785,452

DATE: 07/22/2004

TIME: 09:58:14

Input Set : D:\CFR sequence listing.txt

Output Set: N:\CRF4\07222004\J785452.raw

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:14 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:28 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0 ✓
L:103 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0 ✓
L:206 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:0 ✓
L:206 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3 ✓
L:207 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3 ✓
L:220 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0 ✓
L:271 M:112 C: (48) String data converted to lower case, ✓
L:283 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4 ✓
L:285 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213> ✓
ORGANISM:Artificial Sequence ✓
L:285 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:285 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:0 ✓
L:285 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:285 ✓
L:297 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5 ✓
L:299 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213> ✓
ORGANISM:Artificial Sequence
L:299 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:299 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:0
L:299 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:299
L:310 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6 ✓
L:312 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:312 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:312 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:0
L:312 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:312
L:323 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7 ✓
L:325 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:325 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:325 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:0
L:325 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:325
L:336 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8 ✓
L:338 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:338 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:338 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:0
L:338 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:338
L:349 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9 ✓
L:351 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213> ✓
ORGANISM:Artificial Sequence
L:351 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:351 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:0
L:351 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:351
L:362 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10 ✓
L:364 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>

ORGANISM:Artificial Sequence

L:364 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>

ORGANISM:Artificial Sequence

L:364 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:0

L:364 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:364

L:375 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11

L:377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213>

ORGANISM:Artificial Sequence

L:377 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>

ORGANISM:Artificial Sequence

L:377 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:11 differs:0

VERIFICATION SUMMARY

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L:377 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11, Line#:377 ✓
L:388 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:0, <213> ✓
ORGANISM:Artificial Sequence
L:390 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:0, <213>
ORGANISM:Artificial Sequence
L:390 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:0 ✓
L:390 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12, Line#:390